

Box 509, 1642

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

RECEIVED

MAY 25 2001

TECH CENTER 1600/2900

#101A  
KD  
5-30-01

In re application of

Yoji IKAWA et al.

Appln. No.: 09/670,568

Confirmation No.: Unassigned

Filed: September 27, 2000

Group Art Unit: 1642

Examiner: N. Davis

For: HUMAN P51 GENES AND GENE PRODUCTS THEREOF

**RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

This response is in reference to the Notice to Comply, mailed April 27, 2001, issued in the above referenced patent application. As the Notice was mailed April 27, 2001, and set a one month period for response, this response is timely filed as it is being filed on or before May 27, 2001.

In the Notice, the Examiner states that the Sequence Listing previously submitted in this application fails to comply with the requirements of 37 C.F.R. §§1.821-1.825 for the reasons set forth in the attached Notice to Comply and Raw Sequence Listing Error Report.

The Error Report indicates that one line of amino acid sequence is missing from SEQ ID NO: 5. Applicants have corrected the error in the amended Sequence Listing submitted herewith.



**RESPONSE TO NOTICE TO COMPLY**

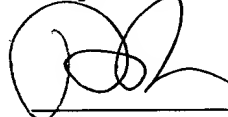
**Q61014**

In addition to the present Response to Notice to Comply, Applicants file herewith a paper copy and copy in computer readable form of the Sequencing Listing, a Statement to Support Filing and Submission in Accordance with 37 C.F.R. §§1.821-1.825, and a copy of the Notice.

Applicants assert that the Response to Notice to Comply and the enclosures are being timely filed, and that the enclosures bring the present application in full compliance with the requirements of 37 C.F.R. §§1.821-1.825.

Accordingly, Applicants respectfully request that the Examiner acknowledge that the Sequence Listing in the present application meets the requirements of 37 C.F.R. §§1.821-1.825.

Respectfully submitted,



Drew Hissong  
Registration No. 44,765

SUGHRUE, MION, ZINN,  
MACPEAK & SEAS, PLLC  
2100 Pennsylvania Avenue, N.W.  
Washington, D.C. 20037-3213  
Telephone: (202) 293-7060  
Facsimile: (202) 293-7860

Date: May 24, 2001

# Notice to Comply

Application No.

09/670568

Applicant(s)

Examiner

Art Unit

## NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

### Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

**RECEIVED**

MAY 25 2001

TECH CENTER 1600/2900

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Yoji IKAWA et al.

Appln. No.: 09/670,568

Confirmation No.: Unassigned

Group Art Unit: 1642

Filed: September 27, 2000

Examiner: N. Davis

For: HUMAN P51 GENES AND GENE PRODUCTS THEREOF

**STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825**

Assistant Commissioner for Patents  
Washington, D.C. 20231  
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include any new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by



**STATEMENT TO SUPPORT FILING AND SUBMISSION  
IN ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825**

**Q61014**

fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,



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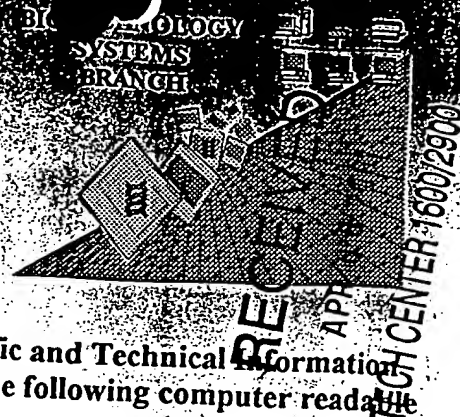
Drew Hissong  
Registration No. 44,765

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Washington, D.C. 20037-3213  
Telephone: (202) 293-7060  
Facsimile: (202) 293-7860

Date: May 24, 2001

# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,568

Source: 1642

Date Processed by STIC: 3/29/2001

BEST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR 1.821-1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errors in sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

1642

## RAW SEQUENCE LISTING

DATE: 03/29/2001

PATENT APPLICATION: US/09/670,568

TIME: 10:20:49

Input Set : A:\sequence listing (p99-16).txt

Output Set: N:\CRF3\03292001\I670568.raw

Does Not Comply  
Corrected Diskette Needed

119> APPLICANT: Ikawa, Yoji  
 4 Otsuka Pharmaceutical Co. Ltd.  
 6 <20> TITLE OF INVENTION: Human p51 gene and its product  
 130> FILE REFERENCE: P99-16  
 9 <140> CURRENT APPLICATION NUMBER:  
 10 <141> CURRENT FILING DATE: 2000-09-27  
 12 <150> PRIOR APPLICATION NUMBER: JP P1998-100467  
 13 <151> PRIOR FILING DATE: 1998-03-27  
 15 <160> NUMBER OF SEQ ID NOS: 23  
 17 <170> SOFTWARE: PatentIn Ver.2.0

## ERRORED SEQUENCES

389 <210> SEQ ID NO: 5  
 390 <211> LENGTH: 2270  
 391 <212> TYPE: DNA  
 392 <213> ORGANISM: Human  
 394 <220> FEATURE:  
 395 <221> NAME/KEY: CDS  
 396 <222> LOCATION: (145)..(2067)  
 398 <400> SEQUENCE: 5  
 399 tcgttgatat caaagacagt tgaaggaaat gaattttgaa acttcacggt gtgccaccct 60  
 400 acagtactgc cctgaccctt acatccagcg ttctgtagaa acccagctca tttctcttgg 120  
 401 aaagaaagtt attaccgata cacc atg tcc cag agc aca cag aca aat gaa 171  
 402 Met Ser Gln Ser Thr Gln Thr Asn Glu  
 403 1 5  
 404 ttc ctc agt cca gag gtt ttc cag cat atc tgg gat ttt ctg gaa cag 219  
 405 Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln  
 406 10 15 20 25  
 407 cct ata tgt tca gtt cag ccc att gac ttg aac ttt gtg gat gaa cca 267  
 408 Pro Ile Cys Ser Val Gln Pro Ile Asp Leu Asn Phe Val Asp Glu Pro  
 409 30 35 40  
 410 tca gaa gat ggt gcg aca aac aag att gag att agc atg gac tgt atc 315  
 411 Ser Glu Asp Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile  
 412 45 50 55  
 413 cgc atg cag gac tcg gac ctg agt gac ccc atg tgg cca cag tac acg 363  
 414 Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr  
 415 60 65 70  
 416 aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc 411  
 417 Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser  
 418 75 80 85  
 419 tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc gtc acg 459  
 420 Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr  
 421 90 95 100 105  
 422 gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct ctc tct 507  
 423 Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser

## RAW SEQUENCE LISTING

DATE: 03/29/2001

PATENT APPLICATION: US/09/670,568

TIME: 10:20:49

Input Set : A:\sequence listing (p99-16).txt

Output Set: N:\CRF3\03292001\I670568.raw

424				110				115				120					
425	cca	tca	ccc	gcc	atc	ccc	tcc	aac	acc	gac	tac	cca	ggc	ccg	cac	agt	555
426	Pro	Ser	Pro	Ala	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	
427				125				130				135					
428	ttc	gac	gtg	tcc	ttc	cag	cag	tcg	agc	acc	gcc	aag	tcg	gcc	acc	tg	603
429	Phe	Asp	Val	Ser	Phe	Gln	Gln	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp		
430			140					145				150					
431	acg	tat	tcc	act	gaa	ctg	aag	aaa	ctc	tac	tgc	caa	att	gca	aag	aca	651
432	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	
433		155				160				165							
434	tgc	ccc	atc	cag	atc	aag	gtg	atg	acc	cca	cct	cct	cag	gga	gct	gtt	699
435	Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Gln	Gly	Ala	Val		
436	170					175				180				185			
437	atc	cgc	gcc	atg	cct	gtc	tac	aaa	aaa	gct	gag	cac	gtc	acg	gag	gtg	747
438	Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	
439				190				195				200					
440	gtg	aag	cgg	tgc	ccc	aac	cat	gag	ctg	agc	cgt	gaa	ttc	aac	gag	gga	795
441	Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	
442			205					210				215					
443	cag	att	gcc	cct	cct	agt	cat	ttg	att	cga	gta	gag	ggg	aac	agc	cat	843
444	Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	
445		220				225				230							
446	gcc	cag	tat	gta	gaa	gat	ccc	atc	aca	gga	aga	cag	agt	gtg	ctg	gta	891
447	Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	
448		235				240				245							
449	cct	tat	gag	cca	ccc	cag	gtt	ggc	act	gaa	ttc	acg	aca	gtc	ttg	tac	939
450	Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	
451	250					255				260				265			
452	aat	ttc	atg	tgt	aac	agc	agt	tgt	gtt	gga	ggg	atg	aac	cgc	cgt	cca	987
453	Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	
454			270					275				280					
455	att	tta	atc	att	gtt	act	ctg	gaa	acc	aga	gat	ggg	caa	gtc	ctg	ggc	1035
456	Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	
457		285				290						295					
458	cga	cgc	tgc	ttt	gag	gcc	cgg	atc	tgt	gct	tgc	cca	gga	aga	gac	agg	1083
459	Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	
460		300				305				310							
461	aag	gcg	gat	gaa	gat	agc	atc	aga	aag	cag	caa	gtt	tcg	gac	agt	aca	1131
462	Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr	
463		315				320				325							
464	aag	aac	ggt	gat	ggt	acg	aag	cgc	ccg	ttt	cgt	cag	aac	aca	cat	ggt	1179
465	Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly	
466	330					335				340				345			
467	atc	cag	atg	aca	tcc	atc	aag	aaa	cga	aga	tcc	cca	gat	gat	gaa	ctg	1227
468	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu	
469			350					355				360					
470	tta	tac	tta	cca	gtg	agg	ggc	cgt	gag	act	tat	gaa	atg	ctg	ttg	aag	1275
471	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys	
472			365					370				375					



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/670,568

DATE: 03/29/2001  
TIME: 10:20:49

Input Set : A:\sequence listing (p99-16).txt  
Output Set: N:\CRF3\03292001\I670568.raw

473 atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac aca att 1323  
474 Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile  
475 380 385 390  
476 gaa acg tac agg caa cag caa cag cag cag cac cag cac tta ctt cag 1371  
E--> 477 395 400 405  
478 aaa cag acc tca ata cag tct cca tct tca tat ggt aac agc tcc cca 1419  
479 Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro  
W--> 480 410 415 420 425  
481 cct ctg aac aaa atg aac agc atg aac aag ctg cct tct gtg agc cag 1467  
482 Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln  
W--> 483 430 435 440  
484 ctt atc aac cct cag cag cgc aac gcc ctc act cct aca acc att cct 1515  
485 Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Ile Pro  
W--> 486 445 450 455  
487 gat ggc atg gga gcc aac att ccc atg atg ggc acc cac atg cca atg 1563  
488 Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met  
W--> 489 460 465 470  
490 gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct ccc cca 1611  
491 Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro  
W--> 492 475 480 485  
493 ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg tat ccc 1659  
494 Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro  
W--> 495 490 495 500 505  
496 aca gat tgc agc att gtc agt ttc tta ggc agg ttg ggc tgt tca tca 1707  
497 Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser  
W--> 498 510 515 520  
499 tgt ctg gac tat ttc acg acc cag ggc ctg acc acc atc tat cag att 1755  
500 Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile  
W--> 501 525 530 535  
502 gag cat tac tcc atg gat gat ctg gca agt ctg aaa atc cct gag caa 1803  
503 Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln  
W--> 504 540 545 550  
505 ttt cga cat gcg atc tgg aag ggc atc ctg gac cac cgg cag ctc cac 1851  
506 Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His  
W--> 507 555 560 565  
508 gaa ttc tcc tcc cct tct cat ctc ctg cgg acc cca agc agt gcc tct 1899  
509 Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser  
W--> 510 570 575 580 585  
511 aca gtc agt gtg ggc tcc agt gag acc cgg ggt gag cgt gtt att gat 1947  
512 Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp  
W--> 513 590 595 600  
514 gct gtg cga ttc acc ctc cgc cag acc atc tct ttc cca ccc cga gat 1995  
515 Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp  
W--> 516 605 610 615  
517 gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat aag caa 2043  
518 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Asn Lys Gln  
W--> 519 620 625 630  
520 cag cgc atc aaa gag gag ggg gag tgagcctcac catgtgagct cttcctatcc 2097  
521 Gln Arg Ile Lys Glu Glu Gly Glu

amino acids  
missing  
under triplets

## RAW SEQUENCE LISTING

DATE: 03/29/2001

PATENT APPLICATION: US/09/670,568

TIME: 10:20:49

Input Set : A:\sequence listing (p99-16).txt

Output Set: N:\CRF3\03292001\I670568.raw

④ > 522            635                            640  
523 ctctcctaac tgccagcccc ctaaaagcac tcctgcttaa tcttcaaagc cttctcccta 2157  
524 gctcctcccc ttctcttgt ctgatttctt aggggaagga gaagtaagag gctacctctt 2217  
525 acctaacatc tgacctggca tctaattctg attctggctt taagccttca aaa 2270

## VERIFICATION SUMMARY

DATE: 03/29/2001

PATENT APPLICATION: US/09/670,568

TIME: 10:20:50

Input Set : A:\sequence listing (p99-16).txt

Output Set: N:\CRF3\03292001\I670568.raw

L:9 M:283 W: Missing Blank Line separator, <140> field identifier  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:477 M:254 E: No. of Bases conflict, LENGTH:Input:405 Counted:1371 SEQ:5  
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:489 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:495 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:504 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:507 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:513 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:516 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:644 M:283 W: Missing Blank Line separator, <400> field identifier  
L:715 M:283 W: Missing Blank Line separator, <400> field identifier

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